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By: Nancy Ramos Printed: Nancy Ramos

**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

In re Application of: Bandman et al.

Title: HUMAN EXTRACELLULAR MATRIX PROTEINS

Serial No.: To Be Assigned Filing Date: Herewith

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**Official Draftsman**

Commissioner for Patents  
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**SUBMISSION OF FORMAL DRAWINGS**

Sir:

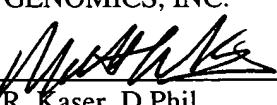
Transmitted herewith are Figure(s) 1A, 1B, 1C, 1D, 1E, 1F, 1G, 2A, 2B, 2C, 2D, 2E, 3A, 3B, 4A, 4B, and 4C, as seventeen (17) sheets of formal drawings for this application. Each sheet of drawing indicates the identifying indicia suggested in 37 CFR Section 1.84(c) on the reverse side of the drawings.

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If there are any questions regarding the above, the Examiner is invited to call the undersigned at 650-855-0555.

Respectfully submitted,

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9	18	27	36	45	54		
CCA AGA TTG TTG TGA GGA GTC TAG CCA GTT GGT GAG CGC TGT AAT CTG AAC CAG							
63	72	81	90	99	108		
C TG TGT CCA GAC TGA GGC CCC ATT TGC ATT ATT TAA CAT ACT TAG AAA ATG AAG							
117	126	135	144	153	162		
TGT TCA TTT TTA ACA TTC CTC CTC CAA TTG GTT TAA TGC TGA ATT ACT GAA GAG							
171	180	189	198	207	216		
GGC TAA GCA AAA CCA GGT GCT TGC GCT GAG GGC TCT GCA GTG GCT GGG AGG ACC							
225	234	243	252	261	270		
CCG GCG CTC TCC CCG TGT CCT CTC CAC GAC TCG CTC GGC CCC TCT GGA ATA AAA							
279	288	297	306	315	324		
CAC CGA GCC CCG AGG GCC CAG AGG CCG ACG TGC CCG AGC TCC TCC TCC GGG							
333	342	351	360	369	378		
GGT CCC GCC CGC GAG CTT TCT TCT CGC CTT CGC ATC TCC TCC TCG CGC GTC TTG							
387	396	405	414	423	432		
GAC ATG CCA CGA ATA AAA AGG ATA CTC ACT GTT ACC ATT CTG GCT CTC TGT CTT	M	P	I	L	A	L	C
			V	T	I		L

FIGURE 1A

CCA	AGC	CCT	GGG	AAT	GCA	CAG	GCA	CAG	TGC	ACG	AAT	GGC	TTT	GAC	CTG	GAT	CGC	486	
P	S	P	G	N	A	Q	A	Q	C	T	N	G	F	D	L	D	R		
441		450		459		468		477		486		495		504		513		522	
CAG	TCA	GGG	CAG	TGT	TTA	GAT	ATT	GAA	TGC	CGA	ACC	ATC	CCC	GAG	GCC	TGC	540		
Q	S	G	Q	C	L	D	I	D	E	C	R	T	I	P	E	A	C		
549		558		567		576		585		594		CGA	GGA	GAC	ATG	ATG	TGT	GTT	
R	G	D	M	M	C	V	N	Q	N	G	G	Y	L	C	I	P	R		
603		612		621		630		639		648		ACA	AAC	CCT	GTG	TAT	CGA	GGG	
T	N	P	V	Y	R	G	P	Y	S	N	P	Y	S	T	P	Y	S		
657		666		675		684		693		702		GGT	CCG	TAC	CCA	GCA	GCT	TCA	
G	P	Y	P	A	A	P	P	L	S	A	P	N	Y	P	T	I			
711		720		729		738		747		756		TCC	AGG	CTT	ATA	TGC	CGC	TTT	
S	R	P	L	I	C	R	F	G	Y	Q	M	D	E	S	N	Q	C		
765		774		783		792		801		810		GTG	GAT	GTG	GAC	GAG	TGT	GCA	
V	D	V	D	E	C	A	T	D	S	H	Q	C	N	P	T	Q	I		

FIGURE 1B

819	TGC ATC AAT ACT GAA GGC GGG TAC ACC TGC TCC ACC GAC GGA TAT TGG CTT	828	837	846	855	864		
C I N T E G C Q C L D I	G Y T C S C T D G Y W L							
873	CCTG GAA GGC CAG TGC TTA GAC ATT GAT GAA TGT CGC TAT GGT TAC TGC CAG CAG	882	891	900	909	918		
L E G Q C A N V P	G S Y D C R Y G C Q							
927	CTC TGT GCG AAT GTT CCT GGA TCC TAT TCT TGT ACA TGC AAC CCT GGT TTT ACC	936	945	954	963	972		
L C A N V P	G S Y D C R Y G C Q							
981	CTC AAT GAG GAT GGA AGG TCT TGC CAA GAT GTG AAC GAG TGT GCC ACC GAG AAC	990	999	1008	1017	1026		
L N E D G R S C Q	V P D V N E C A T E N							
1035	CCC TGC GTG CAA ACC TGC GTC AAC ACC TAC GGC TCT TTC ATC TGC CGC TGT GAC	1044	1053	1062	1071	1080		
P C V Q T C V N T Y G S F I C R C D								
1089	CCA GGA TAT GAA CTT GAG GAA GAT GGC GTT CAT TGC AGT GAT ATG GAC GAG TGC	1098	1107	1116	1125	1134		
P G Y E L F E D G V H C S D M D E C								
1143	AGC TTC TCT GAG TTC CTC TGC CAA CAT GAG TGT GTG AAC CAG CCC GGC ACA TAC	1152	1161	1170	1179	1188		
S F S E F L C Q H E C V N Q P G T Y								

FIGURE 1C

TTC	TGC	TCC	TGC	CCT	CCA	GGC	TAC	ATC	CTG	CTG	GAT	GAC	AAC	CGA	AGC	TGC	CAA		1242
F	C	S	C	P	P	G	Y	I	L	L	D	D	N	R	S	C	Q		
1197		1206		1215		1224		1233		1242									
GAC	ATC	AAC	GAA	TGT	GAG	CAC	AGG	AAC	CAC	ACG	TGC	AAC	CTG	CAG	CAG	ACG	TGC		1296
D	I	N	E	C	E	H	R	N	H	T	C	N	L	Q	Q	T	C		
1251		1260		1269		1278		1287		1296									
TAC	AAT	TTA	CAA	GGG	GGC	TTC	AAA	TGC	ATC	GAC	CCC	ATC	CGC	TGT	GAG	GAG	CCT		1350
Y	N	L	Q	G	G	F	K	C	I	D	P	I	R	C	E	E	P		
1305		1314		1323		1332		1341		1350									
TAT	CTG	AGG	ATC	AGT	GAT	AAC	CGC	TGT	ATG	TGT	CCT	GCT	GAG	AAC	CCT	GGC	TGC		1404
Y	L	R	I	S	D	N	R	C	M	C	P	A	E	N	P	G	C		
1359		1368		1377		1386		1395		1404									
AGA	GAC	CAG	CCC	TTT	ACC	ATC	TTG	TAC	CGG	GAC	ATG	GAC	GTG	GTG	TCA	GGA	CGC		1458
R	D	Q	P	F	T	I	L	Y	R	D	M	D	V	V	S	G	R		
1413		1422		1431		1440		1449		1458									
TCC	GTT	CCC	GCT	GAC	ATC	TTC	CAA	ATG	CAA	GCC	ACG	ACC	CGC	TAC	CCT	GGG	GCC		1512
S	V	P	A	D	I	F	Q	M	Q	A	T	T	R	Y	P	G	A		
1467		1476		1485		1494		1503		1512									
TAT	TAC	ATT	TTC	CAG	ATC	AAA	TCT	GGG	AAT	GAG	GGC	AGA	GAA	TTT	TAC	ATG	CGG		1566
Y	Y	I	F	Q	I	K	S	G	N	E	G	R	E	F	Y	M	R		

FIGURE 1D

CAA	ACG	GGC	CCC	ATC	AGT	GCC	ACC	CTG	GTG	ATG	ACA	CGC	CCC	ATC	AAA	GGG	CCC	1620
Q	T	G	P	I	S	A	T	L	V	M	T	R	P	I	K	G	P	
1575	1584			1593			1602			1611								1620
CGG	GAA	ATC	CAG	CTG	GAC	TTG	GAA	ATG	ATC	ACT	GTC	AAC	ACT	GTC	ATC	AAC	TTC	1674
R	E	I	Q	L	D	L	E	M	I	T	V	N	T	V	I	N	F	
1629	1638			1647			1656			1665								1674
AGA	GGC	AGC	TCC	GTG	ATC	CGA	CTG	CGG	ATA	TAT	GTG	TCG	CAG	TAC	CCA	TTC	TGA	1728
R	G	S	S	V	I	R	L	R	I	Y	V	S	Q	Y	P	F		
1683	1692			1701			1710			1719								1728
GCC	TCG	GGC	TGG	AGC	CTC	CGA	CGC	TGC	CTC	TCA	TTG	GCA	CCA	AGG	GAC	AGG	AGA	1737
1737	1746			1755			1764			1773								1782
AGA	GAG	GAA	ATA	ACA	GAG	AGA	ATG	AGA	GCG	ACA	CAG	ACG	TTA	GGC	ATT	TCC	TGC	1791
1791	1800			1809			1818			1827								1836
TGA	ACG	TTT	CCC	CGA	AGA	GTC	AGC	CCC	GAC	TTC	CTG	ACT	CTC	ACC	TGT	ACT	ATT	1845
1845	1854			1863			1872			1881								1890
GCA	GAC	CTG	TCA	CCC	TGC	AGG	ACT	TGC	CAC	CCC	CAG	TTC	CTA	TGA	CAC	AGT	TAT	1899
1899	1908			1917			1926			1935								1944
CAA	AAA	GTA	TTA	TCA	TTG	CTC	CCC	TGA	TAG	AAG	ATT	GTT	GGT	GAA	TTT	TCA	AGG	1953
1953	1962			1971			1980			1989								1998

FIGURE 1E

وَيَعْلَمُ الْجِنَّاتُ وَالْأَرْضَ بِأَنَّهُمْ مُّنْذَرُونَ إِنَّمَا يَنْهَاكُمُ الْمُّنْذَرُ عَنِ الْمُحَرَّمِ مَا تَرَكْتُمْ فِي الْأَرْضِ إِنَّمَا يَنْهَاكُمُ الْمُّنْذَرُ عَنِ الْمُحَرَّمِ مَا تَرَكْتُمْ فِي الْأَرْضِ إِنَّمَا يَنْهَاكُمُ الْمُّنْذَرُ عَنِ الْمُحَرَّمِ مَا تَرَكْتُمْ فِي الْأَرْضِ إِنَّمَا يَنْهَاكُمُ الْمُّنْذَرُ عَنِ الْمُحَرَّمِ مَا تَرَكْتُمْ فِي الْأَرْضِ إِنَّمَا يَنْهَاكُمُ الْمُّنْذَرُ عَنِ الْمُحَرَّمِ مَا تَرَكْتُمْ فِي الْأَرْضِ

2007	2016	2025	2034	2043	2052
CCT TCA GTT TAT TTC CAC TAT TTT CAA AGA AAA TAG ATT AGG TTT GCG GGG GTC					
2061	2070	2079	2088	2097	2106
TGA GTC TAT GTT CAA AGA CTG TGA ACA GCT TGC TGT CAC TTC TTC ACC TCT TCC					
2115	2124	2133	2142	2151	2160
ACT CCT TCT CTC ACT GTG TTA CTG CTT TGC AAA GAC CCG GGA GCT GGC GGG GAA					
2169	2178	2187	2196	2205	2214
CCC TGG GAG TAG CTA GTT TGC TTT TTG CGT ACA CAG AGA AGG CTA TGT AAA CAA					
2223	2232	2241	2250	2259	2268
ACC ACA GCA GGA TCG AAG GGT TTT TAG AGA ATG TGT TTC AAA ACC ATG CCT GGT					
2277	2286	2295	2304	2313	2322
ATT TTC AAC CAT AAA AGA AGT TTC AGT TGT CCT TAA ATT TGT ATA ACG GTT TAA					
2331	2340	2349	2358	2367	2376
TTC TGT CTT GTT CAT TTT GAG TAT TTT TAA AAA ATA TGT CGT AGA ATT CCT TCG					
2385	2394	2403	2412	2421	2430
AAA GGC CTT CAG ACA CAT GCT ATG TTC TGT CTT CCC AAA CCC AGT CTC CTC TCC					
2439	2448	2457	2466	2475	2484
ATT TTA GCC CAG TGT TTT CTT TGA GGA CCC CTT AAT CTT GCT TTC TTT AGA ATT					

FIGURE 1F

FIGURE 1G

2493      2502      2511      2520      2529      2538  
TTT ACC CAA TTG GAT TGG AAT GCA GAG GTC TCC AAA CTG ATT AAA TAT TTG AAG  
  
2547  
AGA AAA AAA AAA

FIGURE 2A

FIGURE 2B

GAG	ATT	GGA	TAT	TCC	CGC	TGC	TGC	CAC	TGC	CGC	AGC	CAC	ACA	AAC	CGC	CTA	GAG		810
E	I	G	Y	S	R	C	C	H	C	R	S	H	T	N	R	L	E		
765				774				783			792				801				
TGT	GCC	AAA	CTT	GTG	TGG	GAG	GAA	GCA	ATG	AGC	CGA	TTC	TGT	GAG	GCC	GAG	TTC		864
C	A	K	L	V	W	E	E	A	M	S	R	F	C	E	A	E	F		
819				828				837			846				855				
TCG	GTC	AAG	ACC	CGA	CCC	CAC	TGG	TGC	ACG	CGG	CAG	GGG	GAG	GCT	CGG	TTC		918	
S	V	K	T	R	P	H	W	C	C	T	R	Q	G	E	A	R	F		
873				882				891			900				909				
TCC	TGC	TTC	CAG	GAG	GAA	GCT	CCC	CAG	CCA	CAC	TAC	CAG	CTC	CGG	GCC	TGC	CCC		
S	C	F	Q	E	E	A	P	Q	P	H	Y	Q	L	R	A	C	P		
927				936				945			954				963				
AGC	CAT	CAG	CCT	GAT	ATT	TCC	TGC	GGT	CTT	GAG	CTG	CCT	TTC	CCT	CCT	GGG	GGG	TTC	
S	H	Q	P	D	I	S	S	G	L	E	P	F	P	P	G	V			
981				990				999			1008				1017				
CCC	ACA	TTG	GAC	AAT	ATC	AAG	AAC	ATC	TGC	CAC	CTG	AGG	CGC	TTC	TCT	CGC	TCT	GTG	
P	T	L	D	N	I	K	N	I	C	H	L	R	R	F	R	S	V		
1035				1044				1053			1062				1071				
CCA	CGC	AAC	CTG	CCA	GCT	ACT	GAC	CCC	CTA	CAA	AGG	GAG	CTG	CTG	GCA	CTG	ATC		1134
P	R	N	L	P	A	T	D	P	L	Q	R	E	L	L	A	L	I		

FIGURE 2C

Q	L	E	R	E	F	Q	R	C	C	R	Q	G	N	N	H	T	C		1188
CAG	CTG	GAG	AGG	GAG	TTC	CAG	CGC	TGC	TGC	CGC	CAG	GGG	AAC	AAT	CAC	ACC	TGT		1143
T	W	K	A	W	E	D	T	L	D	K	Y	C	D	R	E	Y	A		1197
V	K	T	H	H	H	L	C	C	R	H	P	P	S	P	T	R	D		1206
GAG	TGC	TTT	GCC	CGT	CCT	GCT	TAC	CCC	AAC	TAT	GAC	CGG	GAC	ATC	CGG	GAT		1251	
E	C	F	A	R	R	A	P	Y	P	N	Y	D	R	D	I	L	T		1260
ATT	GAC	ATC	GGT	CGA	GTC	ACC	CCC	AAC	CTC	ATG	GGC	CAC	CTC	TGT	GGA	AAC	CAA		1305
I	D	I	G	R	V	T	P	N	L	M	G	H	L	C	G	N	Q		1314
AGA	GTT	CTC	ACC	AAG	CAT	AAA	CAT	ATT	CCT	GGG	CTG	ATC	CAC	AAC	ATG	ACT	GCC		1359
R	V	L	T	K	H	K	H	I	P	G	L	I	H	N	M	T	A		1368
CGC	TGC	TGT	GAC	CTG	CCA	TTT	CCA	GAA	CAG	GCC	TGC	TGT	GCA	GAG	GAG	GAG	AAA		1413
R	C	C	D	L	P	F	P	E	Q	A	C	C	A	E	E	E	K		1422
																		1467	
																		1476	
																		1485	
																		1494	
																		1503	
																		1512	

FIGURE 2D

FIGURE 2E

100 90 80 70 60 50 40 30 20 10

1	M P G I K R I L T V T I L A L C L P S P	45517
1	M A T S G V L P G G G F V A S A A A V A	GI 458228
21	G N A Q A Q C T N G F D L D R Q S G Q C	45517
21	G P E M Q T G R N N F V I R R N P A D -	GI 458228
41	L D I D E C R T I P E A C R G D M M C V	45517
40	- -	GI 458228
61	N Q N G G Y L C I P R T N P V Y R G P Y	45517
40	- -	GI 458228
81	S N P Y S T P Y S G P Y P A A A P P L S	45517
40	- -	GI 458228
101	A P N Y P T I S R P L I C R F G Y Q M D	45517
43	I P S N P - - S H R I Q C A A G Y E Q S	GI 458228
121	E S N O C V D V D E C A T D S H Q C N P	45517
61	E H N V C Q D I D E C T A G T H N C R A	GI 458228
141	T Q I C I N T E G G Y T C S C T D G Y W	45517
81	D Q V C I N L R G S F A C Q C P P G Y Q	GI 458228
161	L L E G Q C L D I D E C R Y G - Y C Q Q	45517
101	K R G E Q C V D I D E C T I P P Y C H Q	GI 458228
180	L C A N V P G S Y S C T C N P G F T L N	45517
121	R C V N T P G S F Y C Q C S P G F Q L A	GI 458228
200	E D G R S C Q D V N E C A T E N P C V Q	45517
141	A N N Y T C V D I N E C D A S N Q C A Q	GI 458228
220	T C V N T Y G S F I C R C D P G Y E L E	45517
161	Q C Y N I L G S F I C Q C N Q G Y E L S	GI 458228

FIGURE 3A

Sequence alignment showing conserved regions.

240	E D G V H C S D M D E C S F S E F L C Q	45517
181	S D R L N C E D I D E C R T S S Y L C Q	GI 458228
260	H E C V N Q P G T Y F C S C P P G Y I L	45517
201	Y Q C V N E P G K F S C M C P Q G Y Q V	GI 458228
280	L D D N R S C Q D I N E C E H R N H T C	45517
221	V R - S R T C Q D I N E C E T T N E - C	GI 458228
300	N L Q Q T C Y N L Q G G F K C I D P I R	45517
239	R E D E M C W N Y H G G F R C Y P R N P	GI 458228
320	C E E P Y L R I S D N R C M C P A E N P	45517
259	C Q D P Y I L T P E N R C V C P V S N A	GI 458228
340	G C R D Q P F T I L Y R D M D V V S G R	45517
279	M C R E L P Q S I V Y K Y M S I R S D R	GI 458228
360	S V P A D I F Q M Q A T T R Y P G A Y Y	45517
299	S V P S D I F Q I Q A T T I Y A N T I N	GI 458228
380	I F Q I K S G N E G R E F Y M R Q T G P	45517
319	T F R I K S G N E N G E F Y L R Q T S P	GI 458228
400	I S A T L V M T R P I K G P R E I Q L D	45517
339	V S A M L V L V K S L S G P R E H I V D	GI 458228
420	L E M I T V N T V I N F R G S S V I R L	45517
359	L E M L T V S S I G T F R T S S V L R L	GI 458228
440	R I Y V S Q Y P F	45517
379	T I I V G P F S F	GI 458228

FIGURE 3B

F 100 S 100 D 100 C 100

1	M G T T A R A A L V L T Y L A V A S A A	1621777
1	M G T V S R A A L I L A C L A L A S A A	GI 496120
21	S E G G F T A T G Q R Q L R P E - - -	1621777
21	S E G A F K A S D Q R E M T P E R L F Q	GI 496120
37	H F Q E V G Y A A P P S P P L S R S L P	1621777
41	H L H E V G Y A A P P S L P Q T R R L R	GI 496120
57	M D H P D S S Q H G P P - F E G Q S Q V	1621777
61	V D H S V T S L H D P P L F E E Q R E V	GI 496120
76	Q P P P P S Q E A T P L Q Q E K L L P A Q	1621777
81	Q P P S S P E D I P V Y E E D W P T F L	GI 496120
96	L P A E K E V G P P L P Q E A V P L Q K	1621777
101	N P N V D K A G P A V P Q E A I P L Q K	GI 496120
116	E L P S L Q - - - - - - - - - H P	1621777
121	E Q P P P Q V H I E Q K E I D P P A Q P	GI 496120
124	N E - - - Q K E G M P A P F G D Q S H P	1621777
141	Q E E I V Q K E V K P H T L A G Q L P P	GI 496120
141	E P E S W N A A Q H C Q Q D R S Q G G W	1621777
161	E P R T W N P A R H C Q Q G R - R G V W	GI 496120
161	G H R L D G F P P G R P S P D N L N Q I	1621777
180	G H R L D G F P P G R P S P D N L K Q I	GI 496120
181	C L P N R Q H V V Y G P W N L P Q S S Y	1621777
200	C L P E R Q H V I Y G P W N L P Q T G Y	GI 496120
201	S H L T R Q G E T L N F L E I G Y S R C	1621777
220	S H L S R Q G E T L N V L E T G Y S R C	GI 496120

FIGURE 4A

PDB ID: 1KQH

221	C H C R S H T N R L E C A K L V W E E A	1621777
240	C P C R S D T N R L D C L K L V W E D A	GI 496120
241	M S R F C E A E F S V K T R P H W C C T	1621777
260	M T Q F C E A E F S V K T R P H L C C R	GI 496120
261	R Q G E A R F S C F Q E E A P Q O P H Y Q	1621777
280	L R G E E R F S C F Q K E A P R P D Y L	GI 496120
281	L R A C P S H Q P D I S S G L E L P F P	1621777
300	L R P C P V H Q N G M S S G P Q L P F P	GI 496120
301	P G V P T L D N I K N I C H L R R F R S	1621777
320	P G L P T P D N V K N I C L L R R F R A	GI 496120
321	V P R N L P A T D P L Q R E L L A L I Q	1621777
340	V P R N L P A T D A I Q R Q L Q A L T R	GI 496120
341	L E R E F Q R C C R Q G N N H T C T W K	1621777
360	L E T E F Q R C C R Q G H N H T C T W K	GI 496120
361	A W E D T L D K Y C D R E Y A V K T H H	1621777
380	A W E G T L D G Y C E R E L A I K T H P	GI 496120
381	H L C C R H P P S P T R D E C F A R R A	1621777
400	H S C C H Y P P S P A R D E C F A H L A	GI 496120
401	P Y P N Y D R D I L T I D I G R V T P N	1621777
420	P Y P N Y D R D I L T L D L S R V T P N	GI 496120
421	L M G H L C G N Q R V L T K H K H I P G	1621777
440	L M G Q L C G S G R V L S K H K Q I P G	GI 496120
441	L I H N M T A R C C D L P F P E Q A C C	1621777
460	L I Q N M T V R C C E L P Y P E Q A C C	GI 496120

FIGURE 4B

461 A E E E K L T F I N D L C G P R R N I W 1621777  
480 G E E E K L A F I E N L C G P R R N S W GI 496120

481 R D P A L C C Y L S P G D E Q V N C F N 1621777  
500 K D P A L C C D L S P E D K Q I N C F N GI 496120

501 I N Y L R N V A L V S G D T E N A K G Q 1621777  
520 T N Y L R N V A L V A G D T G N A T G L GI 496120

521 G E Q G S T G G T N I S S T S E P K E E 1621777  
540 G E Q G P T R G T D A N P A P G S K E E GI 496120

FIGURE 4C